



1632

TECH CENTER 1600/2900

JAN 23 2003

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## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 091667,947  
Source: 1600  
Date Processed by STIC: 01/67/2003

RECEIVED

JAN 23 2003

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name,  
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer-Window, Lobby, Room 1B03, Crystal Plaza Two,  
2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,  
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

## Raw Sequence Listing Error Summary

**ERROR DETECTED****SUGGESTED CORRECTION**

SERIAL NUMBER: 09/667947

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length      Sequence(s)          contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)         . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)      Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence:  
                          (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          (i)       SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                          (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          This sequence is intentionally skipped  
  
                          Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)      Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence.  
                          <210> sequence id number  
                          <400> sequence id number  
                          000
- 9      Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                          Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                          In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10    Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>      Sequence(s)          missing the <220> "Feature" and associated numeric identifiers and responses.  
                          Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                          (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n      n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



Does Not Comply  
Corrected Diskette Needed

1600

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/667,947

DATE: 01/07/2003

TIME: 16:31:43

Input Set : A:\07039-298001.txt

Output Set: N:\CRF4\01072003\I667947.raw

4 <110> APPLICANT: Russell, Stephen James  
 5 Cattaneo, Roberto  
 6 Peng, Kah-Whye  
 7 Schneider, Urs  
 8 Murphy, Anthea L.  
 10 <120> TITLE OF INVENTION: Therapeutic methods and compositions  
 11 using viruses of the recombinant paramyxoviridae family  
 14 <130> FILE REFERENCE: 07039-298001  
 16 <140> CURRENT APPLICATION NUMBER: US 09/667,947  
 C--> 17 <141> CURRENT FILING DATE: 2002-12-18  
 19 <150> PRIOR APPLICATION NUMBER: US 60/155,873  
 20 <151> PRIOR FILING DATE: 1999-09-24  
 22 <160> NUMBER OF SEQ ID NOS: 49  
 24 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 26 <210> SEQ ID NO: 1  
 27 <211> LENGTH: 4  
 28 <212> TYPE: PRT  
 29 <213> ORGANISM: Fragment  
 31 <400> SEQUENCE: 1  
 32 Ile Glu Gly Arg  
 33 1  
 35 <210> SEQ ID NO: 2  
 36 <211> LENGTH: 4  
 37 <212> TYPE: PRT  
 38 <213> ORGANISM: Fragment  
 40 <220> FEATURE:  
 41 <221> NAME/KEY: VARIANT  
 42 <222> LOCATION: 2  
 43 <223> OTHER INFORMATION: Xaa = Any 20 amino acids  
 45 <400> SEQUENCE: 2  
 W--> 46 Arg Xaa Lys Arg  
 47 1  
 49 <210> SEQ ID NO: 3  
 50 <211> LENGTH: 6  
 51 <212> TYPE: PRT  
 52 <213> ORGANISM: Fragment  
 54 <400> SEQUENCE: 3  
 55 Pro Leu Gly Leu Trp Ala  
 56 1 5  
 58 <210> SEQ ID NO: 4  
 59 <211> LENGTH: 6  
 60 <212> TYPE: PRT  
 61 <213> ORGANISM: Fragment

- Invalid responses see error summary sheet  
item 10

The type of errors shown exist throughout  
the Sequence Listing. Please check subsequent  
sequences for similar errors.

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/667,947

DATE: 01/07/2003

TIME: 16:31:43

Input Set : A:\07039-298001.txt

Output Set: N:\CRF4\01072003\I667947.raw

63 <400> SEQUENCE: 4  
64 Tyr Glu Val Asp Gly Trp  
65 1 5  
67 <210> SEQ ID NO: 5  
68 <211> LENGTH: 7  
69 <212> TYPE: PRT  
70 <213> ORGANISM: Fragment  
72 <400> SEQUENCE: 5  
73 Val Asp Val Ala Asp Gly Trp  
74 1 5  
76 <210> SEQ ID NO: 6  
77 <211> LENGTH: 7  
78 <212> TYPE: PRT  
79 <213> ORGANISM: Fragment  
81 <400> SEQUENCE: 6  
82 Val Asp Gln Met Asp Gly Trp  
83 1 5  
85 <210> SEQ ID NO: 7  
86 <211> LENGTH: 6  
87 <212> TYPE: PRT  
88 <213> ORGANISM: Fragment  
90 <400> SEQUENCE: 7  
91 Leu Glu Val Asp Gly Trp  
92 1 5  
94 <210> SEQ ID NO: 8  
95 <211> LENGTH: 6  
96 <212> TYPE: PRT  
97 <213> ORGANISM: Fragment  
99 <400> SEQUENCE: 8  
100 Val Gln Val Asp Gly Trp  
101 1 5  
103 <210> SEQ ID NO: 9  
104 <211> LENGTH: 7  
105 <212> TYPE: PRT  
106 <213> ORGANISM: Fragment  
108 <400> SEQUENCE: 9  
109 Val Asp Gln Val Asp Gly Trp  
110 1 5  
112 <210> SEQ ID NO: 10  
113 <211> LENGTH: 4  
114 <212> TYPE: PRT  
115 <213> ORGANISM: Fragment  
117 <400> SEQUENCE: 10  
118 Arg Gly Leu Thr  
119 1  
121 <210> SEQ ID NO: 11  
122 <211> LENGTH: 17  
123 <212> TYPE: PRT  
124 <213> ORGANISM: Fragment

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/667,947

DATE: 01/07/2003

TIME: 16:31:43

Input Set : A:\07039-298001.txt

Output Set: N:\CRF4\01072003\I667947.raw

```

126 <400> SEQUENCE: 11
127 Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly
128 1 5 10 15
129 Pro
132 <210> SEQ ID NO: 12
133 <211> LENGTH: 34
134 <212> TYPE: PRT
135 <213> ORGANISM: Fragment ✓
137 <400> SEQUENCE: 12
138 Met Ser Pro Gln Arg Asp Arg Ile Asn Ala Phe Tyr Lys Asp Asn Pro
139 1 5 10 15
140 His Pro Lys Gly Ser Arg Ile Val Ile Asn Arg Glu His Leu Met Ile
141 20 25 30
142 Asp Arg
145 <210> SEQ ID NO: 13
146 <211> LENGTH: 33
147 <212> TYPE: PRT
148 <213> ORGANISM: Fragment ✓
150 <400> SEQUENCE: 13
151 Arg Gly Arg Cys Asn Lys Lys Gly Glu Gln Val Gly Met Ser Arg Pro
152 1 5 10 15
153 Gly Leu Lys Pro Asp Leu Thr Gly Thr Ser Lys Ser Tyr Val Arg Ser
154 20 25 30
155 Leu
158 <210> SEQ ID NO: 14
159 <211> LENGTH: 5
160 <212> TYPE: PRT
161 <213> ORGANISM: Fragment ✓
163 <400> SEQUENCE: 14
164 Arg Arg His Lys Arg
165 1 5
167 <210> SEQ ID NO: 15
168 <211> LENGTH: 4
169 <212> TYPE: PRT
170 <213> ORGANISM: Fragment ✓
172 <400> SEQUENCE: 15
173 Arg His Lys Arg
174 1
176 <210> SEQ ID NO: 16
177 <211> LENGTH: 47
178 <212> TYPE: DNA
179 <213> ORGANISM: Artificial Sequence
181 <220> FEATURE:
182 <223> OTHER INFORMATION: Primer
184 <400> SEQUENCE: 16
185 ttttcctttt ggggcccgtt tcatcaacgc ttctgcaggg acccctc
187 <210> SEQ ID NO: 17
188 <211> LENGTH: 56
189 <212> TYPE: DNA

```

47

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/667,947

DATE: 01/07/2003

TIME: 16:31:43

Input Set : A:\07039-298001.txt

Output Set: N:\CRF4\01072003\I667947.raw

```

190 <213> ORGANISM: Artificial Sequence
192 <220> FEATURE:
193 <223> OTHER INFORMATION: Primer
195 <400> SEQUENCE: 17
196 gtccatgCGG cccagccggc cCGattaaag agagaggcag aggacctgca ggtggg      56
198 <210> SEQ ID NO: 18
199 <211> LENGTH: 18
200 <212> TYPE: PRT
201 <213> ORGANISM: Fragment ✓
203 <400> SEQUENCE: 18
204 Val His Ala Ala Gln Pro Ala Arg Leu Lys Arg Glu Ala Glu Asp Leu
205 1          5          10          15
206 Gln Val
209 <210> SEQ ID NO: 19
210 <211> LENGTH: 50
211 <212> TYPE: DNA
212 <213> ORGANISM: Artificial Sequence
214 <220> FEATURE:
215 <223> OTHER INFORMATION: Primer
217 <400> SEQUENCE: 19
218 ttttcctttt gCGgCGgtt tcatcatcaa cGcttctgCa gggaccctc      50
220 <210> SEQ ID NO: 20
221 <211> LENGTH: 59
222 <212> TYPE: DNA
223 <213> ORGANISM: Artificial Sequence
225 <220> FEATURE:
226 <223> OTHER INFORMATION: Primer
228 <400> SEQUENCE: 20
229 gtccatgCGG cccagccggc cGgtggaggc ggttcagagg cagaggacct gcaggtggg      59
231 <210> SEQ ID NO: 21
232 <211> LENGTH: 19
233 <212> TYPE: PRT
234 <213> ORGANISM: Fragment ✓
236 <400> SEQUENCE: 21
237 Val His Ala Ala Gln Pro Ala Gly Gly Gly Gly Ser Glu Ala Glu Asp
238 1          5          10          15
239 Leu Gln Val
242 <210> SEQ ID NO: 22
243 <211> LENGTH: 16
244 <212> TYPE: PRT
245 <213> ORGANISM: Fragment ✓
247 <400> SEQUENCE: 22
248 Arg Gly Arg Cys Asn Lys Lys Gly Glu Gln Gly Met Ser Arg Pro Gly
249 1          5          10          15
251 <210> SEQ ID NO: 23
252 <211> LENGTH: 9
253 <212> TYPE: PRT
254 <213> ORGANISM: Fragment ✓
256 <400> SEQUENCE: 23

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/667,947

DATE: 01/07/2003

TIME: 16:31:43

Input Set : A:\07039-298001.txt

Output Set: N:\CRF4\01072003\I667947.raw

```

257 Arg Gly Arg Cys Asn Lys Lys Gly Glu
258 1 5
260 <210> SEQ ID NO: 24
261 <211> LENGTH: 26
262 <212> TYPE: DNA
263 <213> ORGANISM: Artificial Sequence
265 <220> FEATURE:
266 <223> OTHER INFORMATION: Primer
268 <400> SEQUENCE: 24
269 aaaactgcag actcaaaggt caatgc 26
271 <210> SEQ ID NO: 25
272 <211> LENGTH: 30
273 <212> TYPE: DNA
274 <213> ORGANISM: Artificial Sequence
276 <220> FEATURE:
277 <223> OTHER INFORMATION: Primer
279 <400> SEQUENCE: 25
280 cccttaatta atatacagat ctcaacggat 30
282 <210> SEQ ID NO: 26
283 <211> LENGTH: 31
284 <212> TYPE: DNA
285 <213> ORGANISM: Artificial Sequence
287 <220> FEATURE:
288 <223> OTHER INFORMATION: Primer
290 <400> SEQUENCE: 26
291 ccatcgataa tggccttcta caaagataac c 31
293 <210> SEQ ID NO: 27
294 <211> LENGTH: 33
295 <212> TYPE: DNA
296 <213> ORGANISM: Artificial Sequence
298 <220> FEATURE:
299 <223> OTHER INFORMATION: Primer
301 <400> SEQUENCE: 27
302 ccatcgataa tgagccatcc caagggaagt agg 33
304 <210> SEQ ID NO: 28
305 <211> LENGTH: 33
306 <212> TYPE: DNA
307 <213> ORGANISM: Artificial Sequence
309 <220> FEATURE:
310 <223> OTHER INFORMATION: Primer
312 <400> SEQUENCE: 28
313 ccatcgataa tgaacagaga acatcttatg att 33
315 <210> SEQ ID NO: 29
316 <211> LENGTH: 29
317 <212> TYPE: DNA
318 <213> ORGANISM: Artificial Sequence
320 <220> FEATURE:
321 <223> OTHER INFORMATION: Primer
323 <400> SEQUENCE: 29

```

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/667,947

DATE: 01/07/2003  
TIME: 16:31:44

Input Set : A:\07039-298001.txt  
Output Set: N:\CRF4\01072003\I667947.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; Xaa Pos. 2

Seq#:35; Xaa Pos. 5,6,7

Seq#:36; N Pos. 1,2,3,4,5,6,7,8,9,10,11,12,15,16,17,20



## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/667,947

DATE: 01/07/2003

TIME: 16:31:44

Input Set : A:\07039-298001.txt

Output Set: N:\CRF4\01072003\I667947.raw

L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0  
L:396 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:35  
L:400 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:35  
L:401 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:0  
L:418 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36  
L:422 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36  
L:426 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36  
L:430 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36  
L:434 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36  
L:438 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36  
L:442 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36  
L:446 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36  
L:450 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36  
L:454 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36  
L:458 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36  
L:462 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36  
L:466 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36  
L:467 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:0